

RAW SEQUENCE LISTING

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Application Serial Number: 10/521,940
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DATE: 02/02/2006

PATENT APPLICATION: US/10/521,940

TIME: 13:07:04

Input Set : A:\10-521,940 Sequence Listing.txt

Output Set: N:\CRF4\02022006\J521940.raw

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3 <110> APPLICANT: Takeuchi, Masahiro
4     Yamaji, Noboru
5     Takasaki, Jun
6     Akamatsu, Masahiko
7     Tsunoyama, Kazuhisa
8     Harigai, Masayoshi
10 <120> TITLE OF INVENTION: NOVEL GENES RELATING TO CHRONIC RHEUMATOID ARTHRITIS
12 <130> FILE REFERENCE: Q85885
14 <140> CURRENT APPLICATION NUMBER: 10/521,940
15 <141> CURRENT FILING DATE: 2005-01-21
17 <150> PRIOR APPLICATION NUMBER: PCT/JP03/09180
18 <151> PRIOR FILING DATE: 2003-07-18
20 <150> PRIOR APPLICATION NUMBER: JP 2002-211951
21 <151> PRIOR FILING DATE: 2002-07-22
23 <160> NUMBER OF SEQ ID NOS: 34
25 <170> SOFTWARE: PatentIn version 3.3
27 <210> SEQ ID NO: 1
28 <211> LENGTH: 1074
29 <212> TYPE: DNA
30 <213> ORGANISM: Homo sapiens
33 <220> FEATURE:
34 <221> NAME/KEY: CDS
35 <222> LOCATION: (1)..(1071)
37 <400> SEQUENCE: 1
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39 Met Gln Leu Arg Asn Val Ser Glu Gln Glu Leu Asp Ser Val Ala Met
40 1          5          10          15
42 aag ctc ctt cac caa gta agc aag ctg tgt ggg aag tgc agc ccc act      96
43 Lys Leu Leu His Gln Val Ser Lys Leu Cys Gly Lys Cys Ser Pro Thr
44          20          25          30
46 gac gtg gac atc ctg cag ccc tcc ttc aac ttc ctg tat tgg agc ctt      144
47 Asp Val Asp Ile Leu Gln Pro Ser Phe Asn Phe Leu Tyr Trp Ser Leu
48          35          40          45
50 cat cag acc aca ccc agc agt cag aaa aga gct gct gca gtg ctc ctg      192
51 His Gln Thr Thr Pro Ser Ser Gln Lys Arg Ala Ala Ala Val Leu Leu
52          50          55          60
54 agc agc aca ggc ctg atg gag ctt ctg gag aag atg ctg gcc ctc acc      240
55 Ser Ser Thr Gly Leu Met Glu Leu Leu Glu Lys Met Leu Ala Leu Thr
56 65          70          75          80
58 ttg gca aag gca gat tct ccc agg act gca ctc ctc tgc tct gcc tgg      288
59 Leu Ala Lys Ala Asp Ser Pro Arg Thr Ala Leu Leu Cys Ser Ala Trp
60          85          90          95
62 ctg ctc act gcc tcc ttc tct gcc cag cag cac aag ggc agt ttg cag      336

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63	Leu	Leu	Thr	Ala	Ser	Phe	Ser	Ala	Gln	Gln	His	Lys	Gly	Ser	Leu	Gln	
64				100					105					110			
66	gtt	cac	cag	aca	ctc	tct	gtg	gaa	atg	gac	caa	gta	ttg	aag	gct	ctc	384
67	Val	His	Gln	Thr	Leu	Ser	Val	Glu	Met	Asp	Gln	Val	Leu	Lys	Ala	Leu	
68			115					120					125				
70	agc	ttt	cca	aag	aaa	aag	gct	gca	cta	ctc	tca	gct	gcc	atc	tta	tgc	432
71	Ser	Phe	Pro	Lys	Lys	Lys	Ala	Ala	Leu	Leu	Ser	Ala	Ala	Ile	Leu	Cys	
72		130					135					140					
74	ttc	ctg	cgg	aca	gcc	ctg	cga	caa	agc	ttt	tcc	tct	gcc	ctg	gta	gcc	480
75	Phe	Leu	Arg	Thr	Ala	Leu	Arg	Gln	Ser	Phe	Ser	Ser	Ala	Leu	Val	Ala	
76	145				150					155					160		
78	ctg	gtg	ccc	tca	ggg	gcc	cag	cca	ctg	cca	gcc	acc	aag	gac	act	gtc	528
79	Leu	Val	Pro	Ser	Gly	Ala	Gln	Pro	Leu	Pro	Ala	Thr	Lys	Asp	Thr	Val	
80				165					170				175				
82	cta	gct	cca	ctg	cga	atg	tcg	caa	gtc	cgg	tcc	ctg	gtc	att	ggg	ctg	576
83	Leu	Ala	Pro	Leu	Arg	Met	Ser	Gln	Val	Arg	Ser	Leu	Val	Ile	Gly	Leu	
84			180					185					190				
86	cag	aac	ctc	ctg	gtg	cag	aag	gac	cct	cta	ttg	tcc	cag	gcc	tgt	gtt	624
87	Gln	Asn	Leu	Leu	Val	Gln	Lys	Asp	Pro	Leu	Leu	Ser	Gln	Ala	Cys	Val	
88		195					200					205					
90	ggc	tgc	ctg	gag	gcc	ttg	ctt	gac	tac	ctg	gat	gcc	cgg	agc	cca	gac	672
91	Gly	Cys	Leu	Glu	Ala	Leu	Leu	Asp	Tyr	Leu	Asp	Ala	Arg	Ser	Pro	Asp	
92		210				215					220						
94	att	gct	ctc	cac	gtg	gcc	tcc	cag	cct	tgg	aat	cgg	ttt	ttg	ctg	ttt	720
95	Ile	Ala	Leu	His	Val	Ala	Ser	Gln	Pro	Trp	Asn	Arg	Phe	Leu	Leu	Phe	
96	225				230				235				240				
98	acc	ctc	ttg	gat	gct	gga	gag	aat	tcc	ttc	ctc	aga	cct	gag	att	ttg	768
99	Thr	Leu	Leu	Asp	Ala	Gly	Glu	Asn	Ser	Phe	Leu	Arg	Pro	Glu	Ile	Leu	
100				245				250				255					
102	agg	ctc	atg	acc	ctg	ttt	atg	cgg	tac	cgg	agt	agc	agt	gtc	ctc	tct	816
103	Arg	Leu	Met	Thr	Leu	Phe	Met	Arg	Tyr	Arg	Ser	Ser	Ser	Val	Leu	Ser	
104			260					265				270					
106	cat	gaa	gag	gtg	ggt	gat	gtt	ctg	caa	ggt	gtg	gct	ttg	gct	gac	ctg	864
107	His	Glu	Glu	Val	Gly	Asp	Val	Leu	Gln	Gly	Val	Ala	Leu	Ala	Asp	Leu	
108		275				280					285						
110	tct	acc	ctc	tcg	aac	acc	aca	ctc	cag	gcc	ctg	cat	ggc	ttc	ttc	cag	912
111	Ser	Thr	Leu	Ser	Asn	Thr	Thr	Leu	Gln	Ala	Leu	His	Gly	Phe	Phe	Gln	
112		290				295					300						
114	cag	ctc	cag	agc	atg	gga	cac	ctg	gct	gac	cac	agc	atg	gcc	cag	acc	960
115	Gln	Leu	Gln	Ser	Met	Gly	His	Leu	Ala	Asp	His	Ser	Met	Ala	Gln	Thr	
116	305				310					315				320			
118	ctg	cag	gcc	tcc	ttg	gag	ggc	ctt	ccc	cct	agc	acc	tcc	tca	ggc	cag	1008
119	Leu	Gln	Ala	Ser	Leu	Glu	Gly	Leu	Pro	Pro	Ser	Thr	Ser	Ser	Gly	Gln	
120			325					330				335					
122	cca	ccc	ctg	cag	gac	atg	ctc	tgc	ctg	gga	ggg	gtg	gct	gta	tcc	ctg	1056
123	Pro	Pro	Leu	Gln	Asp	Met	Leu	Cys	Leu	Gly	Gly	Val	Ala	Val	Ser	Leu	
124			340					345				350					
126	tcc	cac	atc	aga	aac	tga											1074
127	Ser	His	Ile	Arg	Asn												

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128          355
131 <210> SEQ ID NO: 2
132 <211> LENGTH: 357
133 <212> TYPE: PRT
134 <213> ORGANISM: Homo sapiens
136 <400> SEQUENCE: 2
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139 1          5          10          15
142 Lys Leu Leu His Gln Val Ser Lys Leu Cys Gly Lys Cys Ser Pro Thr
143          20          25          30
146 Asp Val Asp Ile Leu Gln Pro Ser Phe Asn Phe Leu Tyr Trp Ser Leu
147          35          40          45
150 His Gln Thr Thr Pro Ser Ser Gln Lys Arg Ala Ala Val Leu Leu
151          50          55          60
154 Ser Ser Thr Gly Leu Met Glu Leu Leu Glu Lys Met Leu Ala Leu Thr
155 65          70          75          80
158 Leu Ala Lys Ala Asp Ser Pro Arg Thr Ala Leu Leu Cys Ser Ala Trp
159          85          90          95
162 Leu Leu Thr Ala Ser Phe Ser Ala Gln Gln His Lys Gly Ser Leu Gln
163          100         105         110
166 Val His Gln Thr Leu Ser Val Glu Met Asp Gln Val Leu Lys Ala Leu
167          115         120         125
170 Ser Phe Pro Lys Lys Lys Ala Ala Leu Leu Ser Ala Ala Ile Leu Cys
171          130         135         140
174 Phe Leu Arg Thr Ala Leu Arg Gln Ser Phe Ser Ser Ala Leu Val Ala
175 145         150         155         160
178 Leu Val Pro Ser Gly Ala Gln Pro Leu Pro Ala Thr Lys Asp Thr Val
179          165         170         175
182 Leu Ala Pro Leu Arg Met Ser Gln Val Arg Ser Leu Val Ile Gly Leu
183          180         185         190
186 Gln Asn Leu Leu Val Gln Lys Asp Pro Leu Leu Ser Gln Ala Cys Val
187          195         200         205
190 Gly Cys Leu Glu Ala Leu Leu Asp Tyr Leu Asp Ala Arg Ser Pro Asp
191          210         215         220
194 Ile Ala Leu His Val Ala Ser Gln Pro Trp Asn Arg Phe Leu Leu Phe
195 225         230         235         240
198 Thr Leu Leu Asp Ala Gly Glu Asn Ser Phe Leu Arg Pro Glu Ile Leu
199          245         250         255
202 Arg Leu Met Thr Leu Phe Met Arg Tyr Arg Ser Ser Ser Val Leu Ser
203          260         265         270
206 His Glu Glu Val Gly Asp Val Leu Gln Gly Val Ala Leu Ala Asp Leu
207          275         280         285
210 Ser Thr Leu Ser Asn Thr Thr Leu Gln Ala Leu His Gly Phe Phe Gln
211          290         295         300
214 Gln Leu Gln Ser Met Gly His Leu Ala Asp His Ser Met Ala Gln Thr
215 305         310         315         320
218 Leu Gln Ala Ser Leu Glu Gly Leu Pro Pro Ser Thr Ser Ser Gly Gln
219          325         330         335
222 Pro Pro Leu Gln Asp Met Leu Cys Leu Gly Gly Val Ala Val Ser Leu

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226 Ser His Ile Arg Asn
227          355
230 <210> SEQ ID NO: 3
231 <211> LENGTH: 306
232 <212> TYPE: DNA
233 <213> ORGANISM: Homo sapiens
236 <220> FEATURE:
237 <221> NAME/KEY: CDS
238 <222> LOCATION: (1)..(303)
240 <400> SEQUENCE: 3
241 atg cct aga agg gga cca caa cag act cga cag gat cca ccg gtt ggg      48
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243 1          5          10          15
245 ccc aag gca gga gga agg gcg gcg ccc cca aac tcc cag gac gcc tgc      96
246 Pro Lys Ala Gly Gly Arg Ala Ala Pro Pro Asn Ser Gln Asp Ala Cys
247          20          25          30
249 agc acc ccc cac gcg ccg ctc tcc gcc tct ggg gag cat cct gcc acc      144
250 Ser Thr Pro His Ala Pro Leu Ser Ala Ser Gly Glu His Pro Ala Thr
251          35          40          45
253 ccc cga cac aca cac ccc ggc tac atc ccg cct tct cac gct tgg tca      192
254 Pro Arg His Thr His Pro Gly Tyr Ile Pro Pro Ser His Ala Trp Ser
255          50          55          60
257 ggc gct ctg gag atg tcg gag atc cag gct ttt cct aaa gag tca gga      240
258 Gly Ala Leu Glu Met Ser Glu Ile Gln Ala Phe Pro Lys Glu Ser Gly
259 65          70          75          80
261 ttg gaa ggc gga ctc cca ccg ttt gct gag ctc cac atg aca aca gca      288
262 Leu Glu Gly Gly Leu Pro Pro Phe Ala Glu Leu His Met Thr Thr Ala
263          85          90          95
265 gac gac agg ccg cac tga      306
266 Asp Asp Arg Pro His
267          100
270 <210> SEQ ID NO: 4
271 <211> LENGTH: 101
272 <212> TYPE: PRT
273 <213> ORGANISM: Homo sapiens
275 <400> SEQUENCE: 4
277 Met Pro Arg Arg Gly Pro Gln Gln Thr Arg Gln Asp Pro Pro Val Gly
278 1          5          10          15
281 Pro Lys Ala Gly Gly Arg Ala Ala Pro Pro Asn Ser Gln Asp Ala Cys
282          20          25          30
285 Ser Thr Pro His Ala Pro Leu Ser Ala Ser Gly Glu His Pro Ala Thr
286          35          40          45
289 Pro Arg His Thr His Pro Gly Tyr Ile Pro Pro Ser His Ala Trp Ser
290          50          55          60
293 Gly Ala Leu Glu Met Ser Glu Ile Gln Ala Phe Pro Lys Glu Ser Gly
294 65          70          75          80
297 Leu Glu Gly Gly Leu Pro Pro Phe Ala Glu Leu His Met Thr Thr Ala
298          85          90          95

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301 Asp Asp Arg Pro His
302      100
305 <210> SEQ ID NO: 5
306 <211> LENGTH: 942
307 <212> TYPE: DNA
308 <213> ORGANISM: Homo sapiens
311 <220> FEATURE:
312 <221> NAME/KEY: CDS
313 <222> LOCATION: (1)..(939)
315 <400> SEQUENCE: 5
316 atg ccc tcg gca cag ccg cca ggc cgt ctt cct ggg gag ccg ccg gag      48
317 Met Pro Ser Ala Gln Pro Pro Gly Arg Leu Pro Gly Glu Pro Pro Glu
318 1      5      10      15
320 cgc ggg caa ctg gga gag ggg gcg gtg ccc agt tcc cgg ccc ggc cct      96
321 Arg Gly Gln Leu Gly Glu Gly Ala Val Pro Ser Ser Arg Pro Gly Pro
322      20      25      30
324 ccc cgc gga ggt ggc cac gtc agc gca gcg tcg ctc gga gct cgc ggc      144
325 Pro Arg Gly Gly Gly His Val Ser Ala Ala Ser Leu Gly Ala Arg Gly
326      35      40      45
328 cgg atg ggg aag gcg gcg gcg gcg gtg gcc ttt ggg gcc gaa gtg ggc      192
329 Arg Met Gly Lys Ala Ala Ala Ala Val Ala Phe Gly Ala Glu Val Gly
330      50      55      60
332 gtg cgg ctc gcg ctg ttc gcg gcc ttc ctg gtg acg gag ctg ctc ccc      240
333 Val Arg Leu Ala Leu Phe Ala Ala Phe Leu Val Thr Glu Leu Leu Pro
334 65      70      75      80
336 ccg ttc cag aga ctc atc cag ccg gag gag atg tgg ctc tac cgg aac      288
337 Pro Phe Gln Arg Leu Ile Gln Pro Glu Glu Met Trp Leu Tyr Arg Asn
338      85      90      95
340 ccc tac gtg gag gcg gag tat ttc ccc acc aag ccg atg ttt gtt att      336
341 Pro Tyr Val Glu Ala Glu Tyr Phe Pro Thr Lys Pro Met Phe Val Ile
342      100     105     110
344 gca ttt ctc tct cca ctg tct ctg atc ttc ctg gcc aaa ttt ctc aag      384
345 Ala Phe Leu Ser Pro Leu Ser Leu Ile Phe Leu Ala Lys Phe Leu Lys
346      115     120     125
348 aag gca gac aca aga gac agc aga caa gcc tgc ctg gct gcc agc ctt      432
349 Lys Ala Asp Thr Arg Asp Ser Arg Gln Ala Cys Leu Ala Ala Ser Leu
350      130     135     140
352 gcc ctg gct ctg aat ggc gtc ttt acc aac aca ata aaa ctg atc gta      480
353 Ala Leu Ala Leu Asn Gly Val Phe Thr Asn Thr Ile Lys Leu Ile Val
354 145     150     155     160
356 ggg agg cca cgc cca gat ttc ttc tac cgc tgc ttc cct gat ggg cta      528
357 Gly Arg Pro Arg Pro Asp Phe Phe Tyr Arg Cys Phe Pro Asp Gly Leu
358      165     170     175
360 gcc cat tct gac ttg atg tgt aca ggg gat aag gac gtg gtg aat gag      576
361 Ala His Ser Asp Leu Met Cys Thr Gly Asp Lys Asp Val Val Asn Glu
362      180     185     190
364 ggc cga aag agc ttc ccc agt gga cat tct tcc ttt gca ttt gct ggt      624
365 Gly Arg Lys Ser Phe Pro Ser Gly His Ser Ser Phe Ala Phe Ala Gly
366      195     200     205

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VERIFICATION SUMMARY

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